



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/766,363

DATE: 09/17/2004

TIME: 10:37:11

Input Set : N:\CrF3\RULE60\10766363.raw
 Output Set: N:\CRF4\09172004\J766363.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Gregory, Richard J.
 3 Wills, Ken N.
 4 Maneval, Daniel C.
 5 (ii) TITLE OF INVENTION: Recombinant Adenoviral Vector and
 6 Methods of Use
 7 (iii) NUMBER OF SEQUENCES: 9
 8 (iv) CORRESPONDENCE ADDRESS:

9 (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 10 (B) STREET: Two Embarcadero Center, Eighth Floor
 11 (C) CITY: San Francisco
 12 (D) STATE: California
 13 (E) COUNTRY: USA
 14 (F) ZIP: 94111-3834

15 (v) COMPUTER READABLE FORM:
 16 (A) MEDIUM TYPE: Floppy disk
 17 (B) COMPUTER: IBM PC compatible
 18 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 19 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

20 (vi) CURRENT APPLICATION DATA:
 C--> 21 (A) APPLICATION NUMBER: US/10/766,363
 C--> 22 (B) FILING DATE: 27-Jan-2004
 W--> 27 (C) CLASSIFICATION:

C--> 28 (vii) PRIOR APPLICATION DATA:

W--> 25 (A) APPLICATION NUMBER: US/08/328,673
 26 (B) FILING DATE: 25-Oct-1994
 W--> 29 (A) APPLICATION NUMBER: US 08/142,669
 30 (B) FILING DATE: 25-OCT-1993
 W--> 31 (A) APPLICATION NUMBER: US 08/233,669
 32 (B) FILING DATE: 26-APR-1994

C--> 33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Smith, Timothy S.
 35 (B) REGISTRATION NUMBER: 35,367
 36 (C) REFERENCE/DOCKET NUMBER: 016930-000920US

C--> 37 (ix) TELECOMMUNICATION INFORMATION:

38 (A) TELEPHONE: (415) 576-0200
 39 (B) TELEFAX: (415) 576-0300

40 (2) INFORMATION FOR SEQ ID NO: 1:

41 (i) SEQUENCE CHARACTERISTICS:
 42 (A) LENGTH: 25 base pairs
 43 (B) TYPE: nucleic acid
 44 (C) STRANDEDNESS: single



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45 (D) TOPOLOGY: linear
W--> 46 (ii) MOLECULE TYPE: DNA
47 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
48 CGCCACCGAG GGACCTGAGC GAGTC 25
50 (2) INFORMATION FOR SEQ ID NO: 2:
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 20 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear
W--> 56 (ii) MOLECULE TYPE: DNA
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
58 TTCTGGGAAG GGACAGAAGA 20
60 (2) INFORMATION FOR SEQ ID NO: 3:
61 (i) SEQUENCE CHARACTERISTICS:
62 (A) LENGTH: 25 base pairs
63 (B) TYPE: nucleic acid
64 (C) STRANDEDNESS: single
65 (D) TOPOLOGY: linear
W--> 66 (ii) MOLECULE TYPE: DNA
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
68 CGCGCTAGCT CTGCCCAAA GAGCT 25
70 (2) INFORMATION FOR SEQ ID NO: 4:
71 (i) SEQUENCE CHARACTERISTICS:
72 (A) LENGTH: 39 base pairs
73 (B) TYPE: nucleic acid
74 (C) STRANDEDNESS: single
75 (D) TOPOLOGY: linear
W--> 76 (ii) MOLECULE TYPE: DNA
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
78 CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGGAAAG 39
80 (2) INFORMATION FOR SEQ ID NO: 5:
81 (i) SEQUENCE CHARACTERISTICS:
82 (A) LENGTH: 35 base pairs
83 (B) TYPE: nucleic acid
84 (C) STRANDEDNESS: single
85 (D) TOPOLOGY: linear
W--> 86 (ii) MOLECULE TYPE: DNA
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
88 CGTGCAGCCG CTGGAGGACT TTGAGGATGT CTGTC 35
90 (2) INFORMATION FOR SEQ ID NO: 6:
91 (i) SEQUENCE CHARACTERISTICS:
92 (A) LENGTH: 33 base pairs
93 (B) TYPE: nucleic acid
94 (C) STRANDEDNESS: single
95 (D) TOPOLOGY: linear
W--> 96 (ii) MOLECULE TYPE: DNA
97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
98 CGCTCTAGAG AGACCAGTTA GGAAGTTTC GCA 33

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100 (2) INFORMATION FOR SEQ ID NO: 7:
 101 (i) SEQUENCE CHARACTERISTICS:
 102 (A) LENGTH: 2995 base pairs
 103 (B) TYPE: nucleic acid
 104 (C) STRANDEDNESS: single
 105 (D) TOPOLOGY: linear
 106 (ii) MOLECULE TYPE: cDNA
 107 (ix) FEATURE:
 108 (A) NAME/KEY: CDS
 109 (B) LOCATION: 139..2925
 110 (D) OTHER INFORMATION: /product= "RB"
 111 /note= "retinoblastoma tumor suppressor"
 112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 113 TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTTGTAA CGGGAGTCGG GAGAGGACGG 60
 114 GGGCGTGCCTCC GCGTGCACGC GCGTCGTCCCT CCCCGGCGCT CCTCCACAGC TCGCTGGCTC 120
 115 CCGCCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC 171
 116 Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
 117 1 5 10
 118 ACC GCC GCC GCT GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC 219
 119 Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro
 120 15 20 25
 121 CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT 267
 122 Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
 123 30 35 40
 124 CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA 315
 125 Leu Val Arg Leu Glu Phe Glu Thr Glu Glu Pro Asp Phe Thr Ala
 126 45 50 55
 127 TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG 363
 128 Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
 129 60 65 70 75
 130 TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT 411
 131 Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
 132 80 85 90
 133 ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA 459
 134 Ile Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
 135 95 100 105
 136 GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC 507
 137 Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
 138 110 115 120
 139 ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT 555
 140 Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
 141 125 130 135
 142 ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT 603
 143 Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
 144 140 145 150 155
 145 GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT 651
 146 Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
 147 160 165 170
 148 ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT 699

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149	Ile	Tyr	Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	
150						175				180				185			
151	GCA	TTG	GTG	CTA	AAA	GTT	TCT	TGG	ATC	ACA	TTT	TTA	TTA	GCT	AAA	GGG	747
152	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	
153						190				195				200			
154	GAA	GTA	TTA	CAA	ATG	GAA	GAT	GAT	CTG	GTG	ATT	TCA	TTT	CAG	TTA	ATG	795
155	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	
156						205				210				215			
157	CTA	TGT	GTC	CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	843
158	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	
159						220				225				230		235	
160	AAA	GAA	CCA	TAT	AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	891
161	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	
162						240				245				250			
163	ACA	CCC	AGG	CGA	GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	939
164	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	
165						255				260				265			
166	GAA	AAT	GAT	ACA	AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	987
167	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	
168						270				275				280			
169	AAT	ATA	GAT	GAG	GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	1035
170	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	
171						285				290				295			
172	ATG	AAT	TCT	CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	1083
173	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Gl	
174						300				305				310		315	
175	AAT	CTT	TCT	AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	1131
176	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	
177						320				325				330			
178	GAT	GCA	AGA	TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	1179
179	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	
180						335				340				345			
181	ATA	GAC	AGT	TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	1227
182	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	
183						350				355				360			
184	GAA	GAG	GTG	AAT	GTA	ATT	CTT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	1275
185	Glu	Glu	Val	Asn	Val	Ile	Leu	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	
186						365				370				375			
187	AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	1323
188	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	
189						380				385				390		395	
190	CCT	TCA	GAA	AAT	CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	1371
191	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	
192						400				405				410			
193	AAA	GAA	AGT	ATA	CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	1419
194	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	
195						415				420				425			
196	GAG	AAA	TTT	GCT	AAA	GCT	GTG	GGG	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	1467
197	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	

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198	430	435	440	
199	CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC			1515
200	Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser			
201	445	450	455	
202	ATG CTT AAA TCA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA			1563
203	Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys			
204	460	465	470	475
205	CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT			
206	Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu			
207	480	485	490	
208	GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT			1659
209	Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp			
210	495	500	505	
211	TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA			1707
212	Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu			
213	510	515	520	
214	AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA			1755
215	Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu			
216	525	530	535	
217	GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT			1803
218	Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His			
219	540	545	550	555
220	CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT			
221	Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp			
222	560	565	570	
223	CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA			1899
224	Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu			
225	575	580	585	
226	TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA			1947
227	Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala			
228	590	595	600	
229	GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT			
230	Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr			
231	605	610	615	
232	ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC			2043
233	Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala			
234	620	625	630	635
235	TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT			
236	Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr			
237	640	645	650	
238	AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA			2139
239	Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu			
240	655	660	665	
241	CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT			
242	Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu			
243	670	675	680	
244	TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT			
245	Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His			
246	685	690	695	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/766,363

DATE: 09/17/2004

TIME: 10:37:12

Input Set : N:\Crf3\RULE60\10766363.raw

Output Set: N:\CRF4\09172004\J766363.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:27 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)
L:28 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:31 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:33 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:37 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:46 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:56 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:66 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:76 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:86 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:96 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6